Homework 6

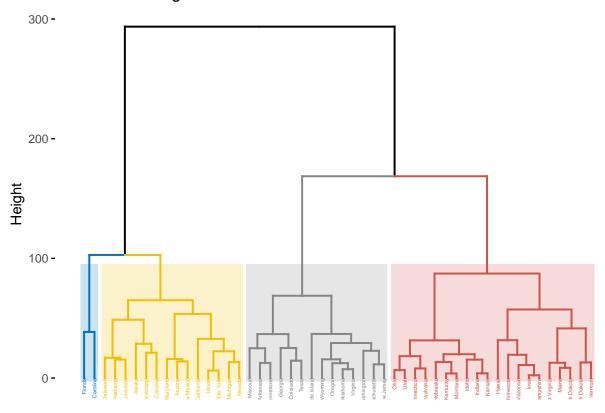
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Cluster analysis

Part A

```
#Querying Dataset
USA <- USArrests
#USA <- scale(USA)
#Hierarchal Clustering
hc.complete <- hclust(dist(USA), method = "complete")</pre>
summary(hc.complete)
               Length Class Mode
## merge
               98 -none- numeric
              49 -none- numeric
## height
           50 -none- numeric
50 -none- character
1 -none- character
## order
## labels
## method
## call
              3 -none- call
## dist.method 1
                      -none- character
fviz_dend(hc.complete,
          k = 4,
          cex = 0.3,
          palette = "jco",
          color_labels_by_k = TRUE,
          #type = c("circular"),
          rect = TRUE,
          rect_fill = TRUE,
          rect_border = "jco",
          labels_track_height = 2.5)
```

Cluster Dendrogram



Part B

```
ind4.complete <- cutree(hc.complete, 3)</pre>
```

List of States in first cluster

```
USA[ind4.complete == 1,] %>% print()
```

##	Murder	Assault	UrbanPop	Rape
## Alabama	13.2	236	58	21.2
## Alaska	10.0	263	48	44.5
## Arizona	8.1	294	80	31.0
## California	9.0	276	91	40.6
## Delaware	5.9	238	72	15.8
## Florida	15.4	335	80	31.9
## Illinois	10.4	249	83	24.0
## Louisiana	15.4	249	66	22.2
## Maryland	11.3	300	67	27.8
## Michigan	12.1	255	74	35.1
## Mississippi	16.1	259	44	17.1
## Nevada	12.2	252	81	46.0
## New Mexico	11.4	285	70	32.1
## New York	11.1	254	86	26.1
## North Carolina	13.0	337	45	16.1

South Carolina 14.4 279 48 22.5

List of States in second cluster

USA[ind4.complete == 2,] %>% print()

##	Murder	Assault	UrbanPop	Rape
## Arkansas	8.8	190	50	19.5
## Colorado	7.9	204	78	38.7
## Georgia	17.4	211	60	25.8
## Massachusetts	4.4	149	85	16.3
## Missouri	9.0	178	70	28.2
## New Jersey	7.4	159	89	18.8
## Oklahoma	6.6	151	68	20.0
## Oregon	4.9	159	67	29.3
## Rhode Island	3.4	174	87	8.3
## Tennessee	13.2	188	59	26.9
## Texas	12.7	201	80	25.5
## Virginia	8.5	156	63	20.7
## Washington	4.0	145	73	26.2
## Wyoming	6.8	161	60	15.6

List of States in third cluster

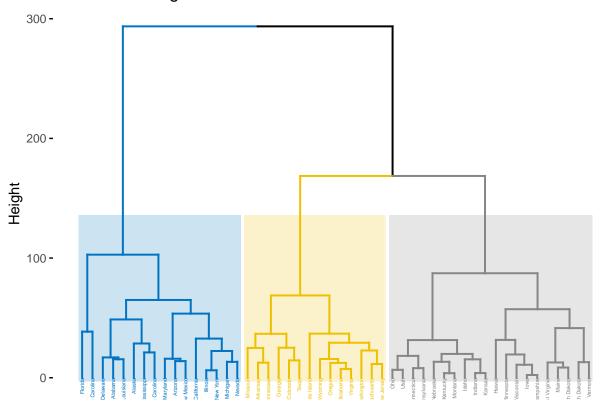
USA[ind4.complete == 3,] %>% print()

##		Murder	Assault	UrbanPop	Rape
##	Connecticut	3.3	110	77	11.1
##	Hawaii	5.3	46	83	20.2
##	Idaho	2.6	120	54	14.2
##	Indiana	7.2	113	65	21.0
##	Iowa	2.2	56	57	11.3
##	Kansas	6.0	115	66	18.0
##	Kentucky	9.7	109	52	16.3
##	Maine	2.1	83	51	7.8
##	Minnesota	2.7	72	66	14.9
##	Montana	6.0	109	53	16.4
##	Nebraska	4.3	102	62	16.5
##	New Hampshire	2.1	57	56	9.5
##	North Dakota	0.8	45	44	7.3
##	Ohio	7.3	120	75	21.4
##	Pennsylvania	6.3	106	72	14.9
##	South Dakota	3.8	86	45	12.8
##	Utah	3.2	120	80	22.9
##	Vermont	2.2	48	32	11.2
##	West Virginia	5.7	81	39	9.3
##	Wisconsin	2.6	53	66	10.8

Dendogram

```
fviz_dend(hc.complete,
    k = 3,
    cex = 0.3,
    palette = "jco",
    color_labels_by_k = TRUE,
    #type = c("circular"),
    rect = TRUE,
    rect_fill = TRUE,
    rect_border = "jco",
    labels_track_height = 2.5)
```

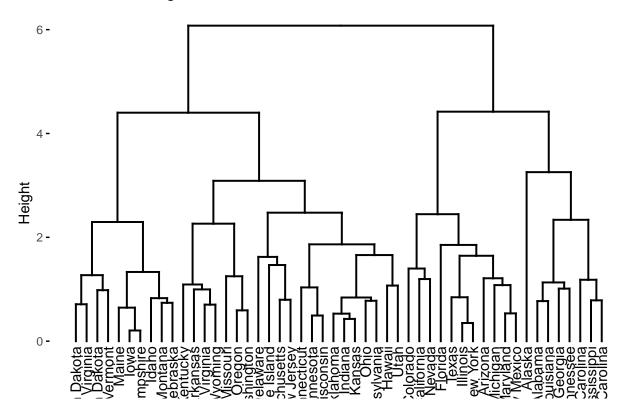
Cluster Dendrogram



Part C

```
USA_scaled <- scale(USA)
scaling <- function(x) (x - mean(x, na.rm = TRUE)) / sd(x, na.rm = TRUE)
hc.complete.scaled <- hclust(dist(USA_scaled), method = "complete")
fviz_dend(hc.complete.scaled) %>% plot()
```

Cluster Dendrogram



Part D:

The goal of the algorithm behind hierarchical clustering is to minimize dissimilarlity between clusters. In this case, scaling resulted in more clusters along with additional tree height. The method we use depends on the nature of the data and the question we are trying to answer. In my opinion, I prefer the more parsimonious model (i.e. pre-scaling). In this case (in my opinion), scaling wasn't as necessary, given that most of the variables were proportions (per 100,000) and another was a percentage.

Problem 2: PCA

```
img <- readJPEG('tiger.jpg')
dim(img)

## [1] 884 884       3

r <- img[,,1]
g <- img[,,2]
b <- img[,,3]

img.r.pca <- prcomp(r, center = FALSE)
img.g.pca <- prcomp(g, center = FALSE)
img.b.pca <- prcomp(b, center = FALSE)</pre>
```

```
rgb.pca <- list(img.r.pca, img.g.pca, img.b.pca)</pre>
# Approximate X with XV_kV_k^T
compress <- function(pr, k)</pre>
{
  compressed.img <- pr$x[,1:k] %*% t(pr$rotation[,1:k])</pre>
  compressed.img
# Using first 20 PCs
pca20 <- sapply(rgb.pca, compress, k = 20, simplify = "array")</pre>
writeJPEG(pca20, "tiger20.jpeg")
# 50 PCS
pca50 <- sapply(rgb.pca, compress, k = 50, simplify = "array")</pre>
writeJPEG(pca50, "tiger50.jpeg")
# 100 PCS
pca100 <- sapply(rgb.pca, compress, k = 100, simplify = "array")</pre>
writeJPEG(pca100, "tiger100.jpeg")
#200 PCS
pca200 <- sapply(rgb.pca, compress, k = 200, simplify = "array")</pre>
writeJPEG(pca200, "tiger200.jpeg")
```

Interpretation:

As the number of principal components increases, so does the clarity of the image. However (in my artistic opinion), the clarity of the image did increase dramatically from 20 to 50 principal components and from 50 to 100 principal components but not so much from 100 to 200 principal components. We need to consider this in real-life applications, especially when figuring out the cut-off for facial recognition software, which has social ramifications.



Figure 1: PCA20

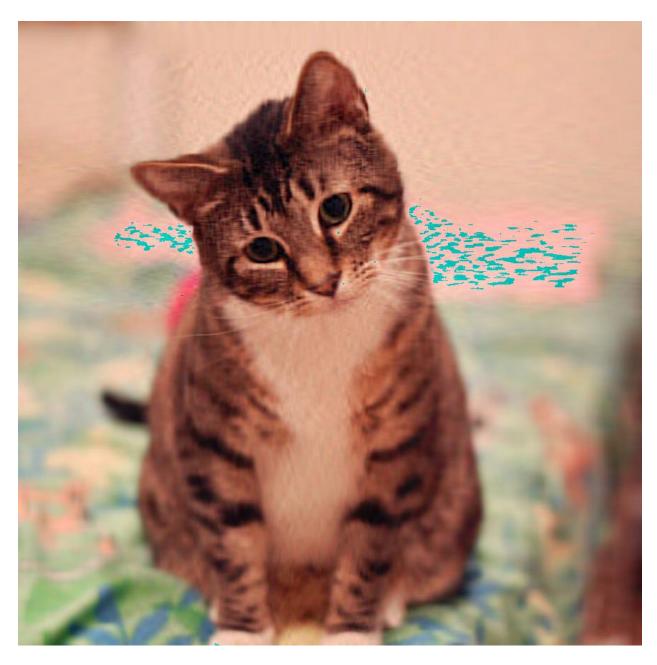


Figure 2: PCA50

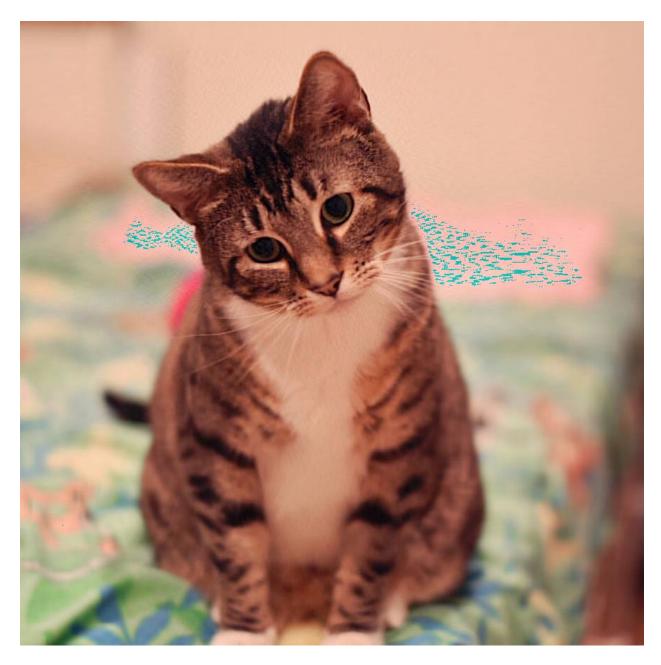


Figure 3: PCA100



Figure 4: PCA200